

Atty. Docket No.  
A33723 070050.1407

Serial No.  
09/911,821

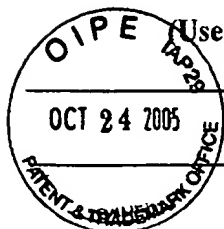
INFORMATION DISCLOSURE STATEMENT  
BY APPLICANT

(Use several sheets if necessary)

Applicant  
Pang et al.

Filing Date  
July 24, 2001

Group Art Unit  
1631



OTHER DOCUMENTS (including Author, Title Date, Pertinent Pages, Etc.)

|     |  |  |   |
|-----|--|--|---|
| EDJ |  |  | Akmaev <i>et al.</i> , "Phylogenetically enhanced statistical tools for RNA structure prediction," 2000, <i>Bioinformatics</i> 16: 501-512.                       |
|     |  |  | Baker, 2000, "A suprising simplicity to protein folding," <i>Nature</i> 405:39-42.  |
|     |  |  | Bateman <i>et al.</i> , 2000, "The Pfam Protein Families Database," <i>Nucleic Acids Research</i> 28:263-266  |
|     |  |  | Jones, "Protein Structure Prediction In the Postgenomic Era," 2000, <i>Current Opinion Structural Biol.</i> 10:371-379.   |
|     |  |  | Phillips <i>et al.</i> , 2000, "Multiple Sequence Alignment in Phylogenetic Analysis," <i>Mol Phylogenet Evol.</i> 16: 317-330.                                   |
|     |  |  | Sanchez <i>et al.</i> , "Protein Structure Modeling for Structural Genomics," 2000, <i>Nature Structural Biology</i> Nov. 2000, Suppl. 986-990.                   |
|     |  |  | Shi and Moore, "The crystal structure of yeast phenylalanine tRNA at 1.93 Angstrom resolution: A classic structure revisited," <i>RNA</i> 2000 Aug 6(8) 1091-105. |
|     |  |  | Lockless and Ranganathan, "Evolutionary Conserved Pathways of Energetic Connectivity," 1999, <i>Science</i> 286:295-299.  |
|     |  |  | Mahalingam <i>et al.</i> , "Structural and kinetic analysis of drug resistant mutants of HIV-1 protease," <i>Eur J Biochem.</i> 1999 263:238-45.                  |
|     |  |  | Olmea <i>et al.</i> , "Effective Use of Sequence Correlation and Conservation in Fold Recognition," 1999, <i>J. Mol. Biol.</i> 293: 1221-1239.                    |
| ✓   |  |  | Pollock <i>et al.</i> , "Coevolving Protein Residues: Maximum Likelihood Identification and Relationship to Structure," 1999, <i>J. Mol. Biol.</i> 287: 187-198.  |

NY02:525956.1

Examiner

*Eui De Jong*

Date Considered

*1/16/2006*

\* Examiner: Initial citation considered, whether or not citation is in conformance with MPEP 609; Draw line through citation if not in conformance and not considered. Include copy of this form with next communication to applicant.

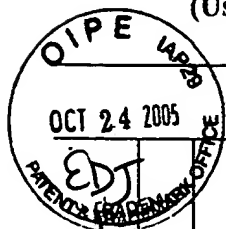
INFORMATION DISCLOSURE STATEMENT  
BY APPLICANT

(Use several sheets if necessary)

Applicant  
Pang et al.

Filing Date  
July 24, 2001

Group Art Unit  
1631



Rost, 1999, "Twilight zone of protein sequence alignments," *Protein Engineering*, 12:85-94.

Konforti *et al.*, "Ribozyme Catalysis from the Major Groove of Group II Intron Domain 5," 1998, *Mol. Cell* 1:433-441.

Puius *et al.*, "Novel Water Mediated Hydrogen Bonds as the Structural Basis for the Low Oxygen Affinity of the Blood Substitute Candidate fHb( $\alpha$ 96VAL->Trp)," 1998, *Biochemistry* 37:9258-65

Sprinzi *et al.* *Nucl. Acids Res.*, "Compilation of tRNA sequences and sequences of tRNA genes," 1998, Vol.26, No.1., 148-153.

Altschul *et al.*, 'Gapped BLAST and PSI-BLAST: a new generation of protein database search programs," *Nucleic Acids Res.* 1997, 25:3389-4302.

Chelvanayagam *et al.*, "An Analysis of simultaneous Variation in protein structure," 1997, *Protein Engineering*. 10:307-316.

Pazos *et al.*, "Correlated Mutations Contain Information About Protein-protein Interaction," 1997, *J. Mol. Biol.* 271: 511-523.

Pollock *et al.*, "Effectiveness of correlation analysis in identifying protein residues undergoing correlated evolution," 1997, *Protein Engineering* 10:647-657.

Agresti, 1996, *An introduction to Categorical Data Analysis*, Wiley, New York., pp16-34.

Rost *et al.*, "Pitfalls of protein sequence analysis," 1996, *Curr. Opin. Biotechnol.* 7:457-461.

Singer *et al.*, "Potential Ligand-Binding Residues in Rat Olfactory Receptors Identified by Correlated Mutation Analysis," 1995, *Receptors and Channels*, 3:89:95.

Neher, 1994, "How frequent are correlated changes in families of protein sequences," *Proc. Natl. Acad. Sci. USA* 91:98-102.

NY02:525956:1

2

Examiner

*Eui De Jong*

Date Considered

*1/17/2006*

\* Examiner: Initial citation considered, whether or not citation is in conformance with MPEP 609; Draw line through citation if not in conformance and not considered. Include copy of this form with next communication to applicant.

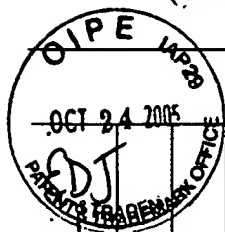
**INFORMATION DISCLOSURE STATEMENT  
BY APPLICANT**

(Use several sheets if necessary)

Applicant  
Pang et al.

Filing Date  
July 24, 2001

Group Art Unit  
1631



Gobel *et al.*, "Correlated Mutations and Residue Contacts in Proteins," 1994, *Proteins: Struct. Funct. Genet.* 18:309-317.

Shindyalov *et al.*, "Can three-dimensional contact in protein structures be predicted by analysis of correlated mutations?" 1994, *Protein Engineering*, 7:349-358.

Taylor *et al.*, "Compensating Changes in Protein Multiple Sequence Alignments," 1994, *Protein Engineering*, 7:341-348.

Agresti, "A Survey of Exact Inference for Contingency Tables," *Statist. Sci.* 7:131-153 1992.

Gutell *et al.*, 1992, "Identifying constraints on the higher-order structure of RNA: continued development and application of comparative sequence analysis methods," *Nucleic Acids Research* 21:5785-5795.

Clarkson *et al.*, "A Remark on Algorithm 643: FEXACT: An Algorithm for Performing Fisher's Exact Test in  $r \times c$  Contingency Tables," *ACM Transactions on Mathematical Software* 19:484-488, 1993.

Korber *et al.*, "Covariation of Mutations in the V3 loop of human immunodeficiency virus type 1 envelope protein: An information theoretic analysis," 1993, *Proc. Natl. Acad. Sci. USA* 90:7176-7180.

Mehta and Patel, "A Network Algorithm For Performing Fisher's Exact Test in  $r \times c$  Contingency Tables," 1983, *J. Am. Stat. Assoc.* 78:427-434.

Duffy, D.E., "A Survey of Exact Inference for Contingency Tables," 1992, *Statistical Science* 7:157-160.

Chiu and Kolodziejczak, "Inferring Consensus Structure From Nucleic Acid Sequences," 1991, *CABIOS*, 7:347-352.

Press *et al.*, 1988-1997, *Numerical Recipes in C. The art of Scientific Computing*. Cambridge University Press, (www.nr.com) Section 6.0-6.2 p212-222, Section 14.4 p628-636.

Altschuh *et al.*, "Correlation of Co-ordinated Amino Acid Substitutions with Function in Viruses Related to Tobacco Mosaic Virus," 1987, *J. Mol. Biol.* 193:693-707.

NY02:525956.1

3

Examiner

*Eui D. Jong*

Date Considered

1/17/2006

\* Examiner: Initial citation considered, whether or not citation is in conformance with MPEP 609; Draw line through citation if not in conformance and not considered. Include copy of this form with next communication to applicant.

Atty. Docket No.  
A33723 070050.1407

Serial No.  
09/911,821

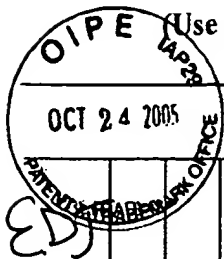
**INFORMATION DISCLOSURE STATEMENT  
BY APPLICANT**

(Use several sheets if necessary)

Applicant  
Pang et al.

Filing Date  
July 24, 2001

Group Art Unit  
1631



Koopmans, 1987, *Introduction to Contemporary Statistical Methods*, Duxbury Press, Boston Chapter 2, p35-69.

Efron, "Nonparametric estimates of standard error: The jackknife, the bootstrap and other methods," 1981, *Biometrika*, 68:589-599.

Patefield, "An Efficient Method of Generating Random R X C Tables With Given Row and Column Totals," *Applied Statistics*, 1981, 30:91-97.

Cochran, "Some Methods For Strengthening The Common X2 Tests," 1954, *Biometrics* 10:417-451.

Cramer, 1946, *Mathematical Methods of Statistics*, Princeton University Press, Princeton, p416-452.

NY02:525956.1

4

Examiner

*Eiri De Jong*

Date Considered

*1/17/2006*

\* Examiner: Initial citation considered, whether or not citation is in conformance with MPEP 609; Draw line through citation if not in conformance and not considered. Include copy of this form with next communication to applicant.